## AMENDMENT TO THE SPECIFICATION

(1) Page 10, first full paragraph,

Figure 10 depicts an amino acid sequence alignment of the *T. reesei* HAC1 (SEQ ID No: 2), *A. nidulans* hacA (SEQ ID No: 4) and *S. cerevisiae* HAC1 (SEQ ID No: 60) proteins. Identical amino acids are shown by asterisks and similar ones by dots. Yeast HAC1 is homologous to the other sequences at the DNA binding domain area. The DNA binding domain is approximately at amino acids 84 – 147 for T. reesei (SEQ ID No: 5) and approximately at amino acids 53 – 116 for A. nidulans (SEQ ID No: 6).

(2) Page 11, first full paragraph,

Figure 16 depicts bandshift experiments, where the binding of the malE-HACI fusion protein to the putative UPR element sequences found in *T. reesei pdi1* and *bip1* promoters was tested. The oligonucleotides used in the binding reactions are shown on the top. Lanes 1, 12 and 16, no protein; lanes 2, 4-7, 8-11, 13-15 and 17-19, malE-HACI fusion protein; lane 3, malE protein alone. The binding was competed with unlabelled oligonucleotides on lanes 5 (20 x excess); lanes 6, 10, 14 and 18 (50 x excess) and lanes 7, 11, 15, and 19 (200 x excess). Alignment of the UPR element sequences that bind the HACI-malE protein is shown below wherein the sequence of pdiUPREII is set forth in SEQ ID No: 61, the sequence of bipUPREI is set forth in SEQ ID No. 62, and the sequence of bipUPREII is set forth in SEQ ID No. 63.